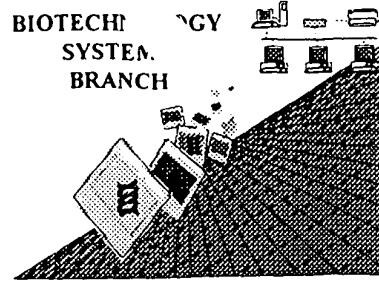


M. Dibr. 3



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/165,546
Source: 1644
Date Processed by STIC: 2-7-01

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/165,546

DATE: 02/07/2001
TIME: 16:09:11

Input Set : A:\#711529 v1 - LUD 5466.4 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02072001\I165546.raw

Does Not Comply
Corrected Diskette Needed
See pp. 1, 2, 3

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 C--> 2 (i) APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
 3 Canlan, Matt; Gure, Ali; Old, Lloyd; Ritter, Gerd
 5 (ii) TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
 6 AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
 7 MHC CLASS I AND MHC CLASS II MOLECULES, AND
 8 USES THEREOF
 10 (iii) NUMBER OF SEQUENCES: 14
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: FULBRIGHT & JAWORSKI LLP
 14 (B) STREET: 666 Fifth Avenue
 15 (C) CITY: New York City
 16 (D) STATE: New York
 17 (E) Country: USA
 18 (F) ZIP: 10158
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 22 (B) COMPUTER: IBM
 23 (C) OPERATING SYSTEM: PC-DOS
 24 (D) SOFTWARE: WordPerfect
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/165,546
 C--> 28 (B) FILING DATE: 02-Oct-1998
 29 (C) CLASSIFICATION: 530
 39 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: 08/937,263
 33 (B) FILING DATE: April 17, 1998
 36 (A) APPLICATION NUMBER: 08/937,263
 37 (B) FILING DATE: September 15, 1997
 40 (A) APPLICATION NUMBER: US 08/752,182
 41 (B) FILING DATE: 03-October-1996
 43 (viii) ATTORNEY/AGENT INFORMATION:
 44 (A) NAME: Hanson, Norman D.
 45 (B) REGISTRATION NUMBER: 30,946
 46 (C) REFERENCE/DOCKET NUMBER: LUD 5466.3
 48 (ix) TELECOMMUNICATION INFORMATION:
 49 (A) TELEPHONE: (212) 688-9200
 50 (B) TELEFAX: (212) 838-3884

ERRORRED SEQUENCES

52 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 752 base pairs
 E--> 55 (B) TYPE: nucleic acid → nucleic acid?

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/165,546

DATE: 02/07/2001
TIME: 16:09:11

Input Set : A:\#711529 v1 - LUD 5466.4 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02072001\I165546.raw

56 (C) STRANDEDNESS: double
57 (D) TOPOLOGY: linear
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 ATCCTCGTGG GCCCTGACCT TCTCTTGAG AGCCGGGCAG AGGCTCCGGA GCC 53
62 ATG CAG GCC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT 98
63 Met Gln Ala Glu Gly Arg Gly Thr Gly Ser Thr Gly Asp Ala
64 5 10 15
66 GAT GGC CCA GGA GGC CCT GGC ATT CCT CAT GGC CCA GGG GGC AAT 143
67 Asp Gly Pro Gly Pro Gly Ile Pro Asp Gly Pro Gly Asn
68 20 25 30
70 GCT GGC GGC CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC 188
71 Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Aly Pro
72 35 40 45
74 CGG GGC GCA GGG GCA GCA AGG GCC TCG GGG CCG GGA GGA GGC GCC 233
75 Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Ala
76 50 55 60
78 CCG CGG GGT CCG CAT GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC 278
79 Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys
80 65 70 75
82 TGC AGA TGC GGG GCC AGG GGG CCG GAG AGC CGC CTG CTT GAG TTC 323
83 Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe
84 80 80 90
86 TAC CTC GCC ATG CCT TTC GCG ACA CCC ATG GAA GCA GAG CTG GCC 368
87 Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala
88 95 100 105
90 CGC AGG AGC CTG GCC CAG GAT GCC CCA CCG CTT CCC GTG CCA GGG 413
91 Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly
92 110 115 120
94 GTG CTT CTG AAG GAG TTC ACT GTG TCC GGC AAC ATA CTG ACT ATC 458
95 Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile
96 125 130 135
98 CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG CAG CTC TCC ATC AGC 503
99 Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser
100 140 145 150
102 TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG ATC ACG CAG TGC 548
103 Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys
104 155 160 165
106 TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG CAG AGG CGC 593
107 Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
108 170 175 180
110 TAA GCCCAGCCTG GCGCCCTTC CTAGGTCTAG CCTCCTCCCC TAGGGAATGG 646
111 TCCCAGCACG AGTGGCCAGT TCATTTGGGG GGCCTGATTG TTTGTCGCTG GAGGAGGACG 706
112 GCTTACATGT TTGTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAAA 752
116 (2) INFORMATION FOR SEQ ID NO: 2:
117 (i) SEQUENCE CHARACTERISTICS:
118 (A) LENGTH: 31 base pairs
E--> 119 (B) TYPE: nuclear acid → *nucleic acid?*
120 (C) STRANDEDNESS: single
121 (D) TOPOLOGY: linear

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/165,546

DATE: 02/07/2001
TIME: 16:09:11

Input Set : A:\#711529 v1 - LUD 5466.4 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02072001\I165546.raw

122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
124 CACACAGGAT CCATGGATGC TGCAGATGCG G 31
128 (2) INFORMATION FOR SEQ ID NO: 3:
129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 32 base pairs
E--> 131 (B) TYPE: nuclear acid → nucleic acid?
132 (C) STRANDEDNESS: single
133 (D) TOPOLOGY: linear
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
136 CACACAAAGC TTGGCTTAGC GCCTCTGCC TG 32
172 (2) INFORMATION FOR SEQ ID NO: 7:
173 (i) SEQUENCE CHARACTERISTICS:
174 (A) LENGTH: 10 amino acids
E--> 175 (B) TYPE: → Delete "semi-colon", replace with "colon" as shown.
176 (D) TOPOLOGY: linear
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
180 Leu Leu Met Trp Ile Thr Gln Cys Phe Leu
181 5 10
209 (2) INFORMATION FOR SEQ ID NO: 10:
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 18 amino acids
E--> 212 (B) TYPE: → Delete "semi-colon", replace with colon as shown.
213 (D) TOPOLOGY: linear
214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
216 Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly
217 5 10 15
219 Asn Ile
264 (2) INFORMATION FOR SEQ ID NO: 14:
265 (i) SEQUENCE CHARACTERISTICS:
266 (A) LENGTH: 6 amino acids
267 (B) TYPE: amino acid
268 (D) TOPOLOGY: linear
E--> 269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
271 Leu Leu Met Trp Ile Thr 5

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VERIFICATION SUMMARY DATE: 02/07/2001
PATENT APPLICATION: US/09/165,546 TIME: 16:09:12

Input Set : A:\#711529 v1 - LUD 5466.4 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02072001\I165546.raw

L:2 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:54 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=1
L:118 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=2
L:130 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=3
L:175 M:220 C: Keyword misspelled or invalid format, [(B) TYPE:]
L:175 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 7, (B) TYPE:
L:174 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=7
L:186 M:220 C: Keyword misspelled or invalid format, [(i) SEQUENCE CHARACTERISTICS:]
L:212 M:220 C: Keyword misspelled or invalid format, [(B) TYPE:]
L:212 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 10, (B) TYPE:
L:211 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=10
L:269 M:212 E: (34) Invalid or duplicate Sequence ID Number, Data=[7:]